

Db 122 SIKRLE 128

RESULT 14
TIML_HUMAN STANDARD: PRT: 207 AA.

AC P01033; Q14252;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid
potential collagenase inhibitor) (Tissue inhibitor of metalloproteinases)
GN TIMP1 OR CLG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RA "SEQUENCE FROM N.A."
RA Doeherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,
RA Harris T.J.R., Murphy G., Reynolds J.J.,
RT "Sequence of human tissue inhibitor of metalloproteinases and its
RT identity to erythroid-potentiating activity."
RL Nature 318:66-69(1985).
RN [2]
RA "SEQUENCE FROM N.A."
RA Gasson J.C., Golde D.W., Kauffman S.E., Westbrook C.A., Hewick R.M.,
RA Kaufman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,
RA Orr E.C., Clark S.C.,
RT "Molecular characterization and expression of the gene encoding human
RT erythroid-potentiating activity."
RL Nature 315:768-771(1985).
RN [3]
RA "SEQUENCE FROM N.A."
RA MEDLINE-86205964; PubMed-3010309;
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.,
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).
RN [4]
RA "SEQUENCE FROM N.A."
RA Kaczorek M., Honore N., Ribes V., Deloux P., Cornet P., Cartwright T.,
RA Streeter R.E.,
RT "Molecular cloning and synthesis of biologically active human tissue
RT inhibitor of metalloproteinases in yeast."
RL Biotechnology 5:595-598(1987).
RN [5]
RA "SEQUENCE FROM N.A."
RA TISSUE-Ovary;
RA MEDLINE-91025550; PubMed-2171551;
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA Scheit K.H.,
RT "Characterization of three abundant mRNAs from human ovarian
RT granulosa cells."
RL DNA Cell Biol. 9:479-485(1990).
RN [6]
RA "SEQUENCE FROM N.A."
RA MEDLINE-94123576; PubMed-7507419;
RA Ophreok A., Kenney M.C., Brown D.,
RT "Characterization of a human corneal metalloproteinase inhibitor
RT (TIMP-1)."
RL Curr. Eye Res. 12:877-883(1993).
RN [7]
RA "SEQUENCE OF 42-207 FROM N.A."
RA Suda T., Kohno K., Kuwano M.,
RT "Cloned and sequenced to the EMBL/GenBank/DBJ databases."
RL OF 1-40 FROM N.A.

RA Harcastle A.J.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [9]
RA DISULFIDE BONDS AND PARTIAL SEQUENCE.
RA MEDLINE-90303199; PubMed-2163605;
RA Williamson R.A., Marton F.A.O., Angal S., Koklitis P., Panico M.,
RA Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;
RT "Disulphide bond assignment in human tissue inhibitor of
RT metalloproteinases (TIMP)."
RL Biochem. J. 268:267-274(1990).
RN [10]
RA "SEQUENCE OF 24-38."
RA TISSUE-Synovial fluid;
RA MEDLINE-92111776; PubMed-1730286;
RA Osthus A., Knauper V., Oberhoff R., Relinke H., Tschesche H.;
RT "Isolation and characterization of tissue inhibitors of
RT metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial
RT fluid."
RL FEBS Lett. 296:16-20(1992).
RN [11]
RA NOTAGENESIS.
RA MEDLINE-93041700; PubMed-1420137;
RA O'Shea M., Willendrook F., Williamson R.A., Cockett M.I.,
RA Freedman R.B., Reynolds J.J., Doeherty A.J.P., Murphy G.;
RT "Site-directed mutations that alter the inhibitory activity of the
RT tissue inhibitor of metalloproteinases-1: Importance of the
RT N-terminal region between cysteine 3 and cysteine 13."
RL Biochemistry 31:10146-10152(1992).
RN [12]
RA X-RAY CRYSTALLOGRAPHY (2.8-ANGSTROMS) OF COMPLEX WITH MMP-3.
RA MEDLINE-97433330; PubMed-9288970;
RA Gomis-Ruth F.X., Maskos K., Betz M., Bergner A., Huber R., Suzuki K.,
RA Yoshida N., Nagase H., Brew K., Bourenkov G.P., Bartunik H., Bode W.,
RT "Mechanism of inhibition of the human matrix metalloproteinase
RT Stromelysin-1 by TIMP-1."
RL Nature 389:77-81(1997).
RN [13]
RA STRUCTURE BY NMR OF 24-149.
RA MEDLINE-20090931; PubMed-10623524;
RA Wu B., Arumugam S., Gao G., Lee G.I., Semchenko V., Huang W.,
RA Brew K., Van Doren S.R.;
RT "NMR structure of tissue inhibitor of metalloproteinases-1 implicates
RT localized induced fit in recognition of matrix metalloproteinases."
RL J. Mol. Biol. 295:257-268(2000).
RN [14]
RA "FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
RA AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIESIS IN
RA VITRO. BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE
RA GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID
RA PROGENITORS. KNOWN TO ACT ON MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,
RA MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 AND MMP-16. DOES NOT ACT ON
RA MMP-14."
RN [15]
RA "SUBCELLULAR LOCATION: Secreted."
RA "PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
RA DISULFIDE BONDS."
RN [16]
RA "SIMILARITY: BELONGS TO THE TIMP FAMILY."
RN [17]
RA "THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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RN [18]
RA EMBL: X03124; CAA26902.1;
RA EMBL: M12670; AAA52436.1;
RA EMBL: X02598; CAA26443.1;
RA EMBL: M59906; AAA63234.1;
RA EMBL: S68252; AAD14009.1;
RA EMBL: D11139; BAA01913.1;
RA EMBL: I47361; AAA75558.1;
RA EMBL: A10416; CAA00898.1;
RA PIR: A01269; ZYHDEP.

PIR: A23534; A23534.
 PIR: A35826; A35826.
 PIR: S20318; S20318.
 DR PDB; 1UEA; 25-NOV-98.
 DR PDB; 1DZB; 22-DEC-99.
 DR GlycoSuiteDB; P01033; .
 DR MIM; 305370; .
 DR InterPro: IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 3D-structure; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT DISULFID 24 93
 FT DISULFID 26 122
 FT DISULFID 36 147
 FT DISULFID 150 197
 FT DISULFID 155 160
 FT DISULFID 168 189
 FT CARBOHYD 53
 FT CARBOHYD 101
 FT CARBOHYD 101
 FT CONFLICT 23 23
 FT CONFLICT 44 44
 FT SEQUENCE 207 AA; 23171 MW; 5A64F90FFAB2ECDC CRC64;

Query Match 1.7%; Score 7; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LINGKLO 52
 DB 107 LINGKLO 113

RESULT 15
 ID TIM1_PAPCY STANDARD; PRT; 207 AA.
 AC P49061;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloprotease inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Papio cynocephalus (Yellow baboon).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 NCBI_TaxID=9536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Aorta;
 RX MEDLINE-96011646; PubMed-7590279;
 RA Prough R., Nikkari S.T., Hasenstab D., Lea H., Clowes A.W.,
 RT "Cloning and characterization of a cDNA encoding the baboon tissue
 RT inhibitor of matrix metalloproteinase-1 (TIMP-1).";
 RL Gene 163:267-271(1995).
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; L37295; AAA9943.1; .
 DR HSSP; P01033; 1UEA.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 3D-structure; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 207
 FT DISULFID 24 93
 FT DISULFID 26 122
 FT DISULFID 36 147
 FT DISULFID 150 197
 FT DISULFID 155 160
 FT DISULFID 168 189
 FT CARBOHYD 53
 FT CARBOHYD 101
 FT CARBOHYD 101
 FT CONFLICT 23 23
 FT CONFLICT 44 44
 FT SEQUENCE 207 AA; 23213 MW; 5A64F90FFAB2ECDC CRC64;

Query Match 1.7%; Score 7; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LINGKLO 52
 DB 107 LINGKLO 113

RESULT 16
 ID MUC3_HUMAN STANDARD; PRT; 213 AA.
 AC 002505; 002506;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Mucin 3A (intestinal mucin 3A) (Fragments).
 GN MUC3A OR MUC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Small intestine;
 RX MEDLINE-90365738; PubMed-2393399;
 RA Gum J.R., Jr., Hicks J.W., Swallow D.M., Lagace R.L., Byrd J.C.,
 RA Lamport D.T.A., Siddiki B., Kim Y.S.,
 RT "Molecular cloning of cDNAs derived from a novel human intestinal
 RT mucin gene.";
 RL Blochem. Biophys. Res. Commun. 171:407-415(1990).
 CC -1- FUNCTION: MAJOR GLYCOPROTEIN COMPONENT OF A VARIETY OF MUCUS GELS.
 CC THOUGHT TO PROVIDE A PROTECTIVE, LUBRICATING BARRIER AGAINST
 CC PARTICLES AND INFECTIOUS AGENTS AT MUCOSAL SURFACES.
 CC -1- TISSUE SPECIFICITY: BROAD SPECIFICITY; SMALL INTESTINE, COLON AND
 CC COLONIC TUMORS.
 CC -1- PTM: HIGHLY O-GLYCOSYLATED AND PROBABLY ALSO N-GLYCOSYLATED.
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 CC EMBL; M55406; AAA63773.1; .
 CC EMBL; M55405; AAA63772.1; .

PR 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YF;

DR WPI: 2001-639362/73.
 N-PSDB; AAS66220.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20; SEQ ID NO 32392; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 332 AA;

Query Match 2.0%; Score 8; DB 22; Length 332;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 381 ELPASSEP 388

DB 160 elpassep 167

RESULT 22

ID ABB65393 standard; Protein; 586 AA.

AC ABB65393;

DI 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 22971.

KW Drosophila: developmental biology; cell signalling; insecticide;

OS Drosophila melanogaster.

PN WO200171042-A2.

22-SEP-2001.

2001; 2001WO-US09231.

2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

N-PSDB; ABL09496.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions

PS Disclosure; SEQ ID NO 22971; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 586 AA;

Query Match 2.0%; Score 8; DB 22; Length 586;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 TALALAST 281

DB 534 talalast 541

RESULT 23

ID AAR51267 standard; Protein; 604 AA.

AC AAR51267;

DI 12-OCT-1994 (first entry)

DE Sequence of human prostaglandin G/H synthase-2 (PGHS-2).

KW Prostaglandin; hormone; eicosanoid; fatty acid metabolism.

OS Homo sapiens.

PN WO9406919-A.

PD 31-MAR-1994.

PF 22-SEP-1993; 93WO-US09167.

PR 22-SEP-1992; 92US-0949780.

PR 01-DEC-1992; 92US-0963835.

PR 22-MAR-1993; 93US-0034143.

PR 28-APR-1993; 93US-0054364.

PA (UYRP) UNIV ROCHESTER.

PI Obanion MK, Winn VD, Young DA;

DR WPI: 1994-118468/14.

DR N-PSDB; AAO61790.

PT New prostaglandin G/H synthase-2 gene - used for producing
 PT transgenic cell lines for testing ability of cpds. to inhibit

Sequence of prostaglandin(s)

claim 40; Page 45-47; 76pp; English.

CC RNA was isolated from a human fibroblast cell line (WI38). PCR
CC primers specific for the human PGHS-1 and PGHS-2 sequences were
CC engineered to amplify the coding regions of either one transcript or
CC the other (see AA061792-95). PCR products of about 2 kb were generated.
CC Three PGHS-2 clones were sequenced in both directions. The clone
CC comprising the PGHS-2 sequence disclosed in AA061790 was selected for
CC transfection. This sequence differs from the human PGHS-2 sequence
CC disclosed by Hla and Hellson, PNAS, 89, 7384 (1992) due to a Glu at
CC this posn.
XX
XX
SQ Sequence 604 AA;

Query Match 2.0%; Score 8; DB 15; Length 604;
Best Local Similarity 100.0%; Pred. No. 65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 SVDPPELI 61
|||||||

Db 567 svdppe1l 574

RESULT 24

AA056660
ID AA056660 standard; Protein; 604 AA.

AC AA056660;

DT 27-FEB-1995 (first entry)

DE Cyclooxygenase-2.

DE Cyclooxygenase-2; enzyme: osteosarcoma; antiinflammatory; assay.

OS Homo sapiens.

XX WO9414977-A.

PD 07-JUL-1994.

PF 17-DEC-1993; 93WO-CA00547.

XX 22-DEC-1992; 92US-0994760.

PR 06-MAY-1993; 93US-0064271.

XX (MERI) MERCK FROST CANADA INC.

PI Cromlish WA, Kennedy BP, Mancini JA, O'Neill G, Vickers PJ;
PI Wong E;

XX WPI: 1994-263635/32.

DR N-PSDB; AA071002.

XX Assays for cyclo:oxygenase-1 and -2 - for identifying selective
XX antagonists, i.e. potential anti inflammatory etc., also new
XX human cyclo:oxygenase-2 and cDNA encoding it

PS Disclosure; Fig 1A-1C; 55pp; English.

XX The human cyclooxygenase-2 COX-2 protein is used in assays to
XX identify inhibitors, which have antiinflammatory, analgesic,
XX antipyretic and anticancer activity.

XX Sequence 604 AA;

Query Match

Best Local Similarity 2.0%; Score 8; DB 15; Length 604;
100.0%; Pred. No. 65;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 SVDPPELI 61
|||||||

Db 567 svdppe1l 574

RESULT 25

AA072228
ID AA072228 standard; Protein; 604 AA.

XX AA072228;

AC 28-SEP-1995 (first entry)

DE Human cyclooxygenase-2.

DE Cyclooxygenase-2; COX-2; COX-1; inhibitor; screening;

KW osteosarcoma.

OS Homo sapiens.

XX WO9509238-A.

PN 06-APR-1995.

PF 13-SEP-1994; 94WO-CA00501.

XX 27-SEP-1993; 93US-0084033.

XX (MERI) MERCK FROST CANADA INC.

PI Mancini JA, O'Neill GP;

XX WPI: 1995-147436/19.

DR N-PSDB; AA089376.

XX High level expression of human cyclo:oxygenase (COX)-2 - using
XX new 3' flanking region from COX-1 useful in assays for
XX identifying potent, selective or preferential inhibitors of COX-2

PS Disclosure; Fig.1; 59pp; English.

XX Full-length cDNA derived from human osteosarcoma cells (given in
XX CC AA089376) encoded human COX-2 (AA072228). High-level expression of
XX COX-2 in COS7 cells was achieved using a vaccinia or baculovirus vector
XX and a construct in which COX-2 cDNA was attached at its 5' end to a 3'

XX flanking sequence of human COX-1 cDNA (AA089377).

XX Sequence 604 AA;

Query Match

Best Local Similarity 2.0%; Score 8; DB 16; Length 604;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 SVDPPELI 61
|||||||

Db 567 svdppe1l 574

RESULT 26

AA012698
ID AA012698 standard; Protein; 604 AA.

XX AA012698;

AC 04-MAY-1997 (first entry)

DE Human prostaglandin H synthase-2.

DE Prostaglandin H synthase-2; PGHS-2; cyclooxygenase; inflammation;
XX pulmonary fibrosis; Alzheimer's disease; stroke; acute head injury;

(FILE 'HOME' ENTERED AT 12:23:55 ON 07 JUN 2002)

FILE 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, DRUGU, DRUGUPDATES, .' ENTERED AT 12:24:16 ON 07 JUN 2002

E REED GUY?/AU

L1

2 S E1 OR E2

E CLEMENT CHRISTOPHE?/AU

L2

7 S E1 OR E2

L3

1752 S PLATELET ACTIVATION PROTEIN OR (APP (A) 2)

L4

0 S L3 (S) (L1 OR L2)

L5

4 S MAB (S) 3B2 (S) PLATELET?

WEST Search History

DATE: Friday, June 07, 2002

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
L6	mab same 3b2 same platelet?	1	L6
L5	L4 and l3	2	L5
L4	platelet activation protein or (app adj 2)	147	L4
L3	L2 or l1	31	L3
L2	clement-christophe-\$.in.	2	L2
L1	reed-guy-\$.in.	29	L1

END OF SEARCH HISTORY